```
          5    10    15    20    25    30    35    40    45
        ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT
        TAC CCA CGT CGA CCT TCT TAC GTT CAC AGA GGA GGG AGG TTT TTC AGA
         M   G   A   G   G   R   M   Q   V   S   P   P   S   K   K   S>

          50    55    60    65    70    75    80    85    90    95
        GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT
        CTT TGG CTG TTG TAG TTC GCG CAT GGG ACG CTC TGT GGC GGG AAG TGA
         E   T   D   N   I   K   R   V   P   C   E   T   P   P   F   T>

          100  105  110  115  120  125  130  135  140
        GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG
        CAG CCT CTT GAG TTC TTT CGT TAG GGT GGC GTG ACA AAG TTT GCG AGC
         V   G   E   L   K   K   A   I   P   P   H   C   F   K   R   S>

         145 150  155  160  165  170  175  180  185  190
        ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC
        TAG GGA GCG AGA AAG AGG ATG GAG TAG ACC CTG TAG TAG TAT CGG AGG
         I   P   R   S   F   S   Y   L   I   W   D   I   I   I   A   S>

         195  200  205  210  215  220  225  230  235  240
        TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT
        ACG AAG ATG ATG CAG CGG TGG TGA ATG AAG GGA GAG GAG GGA GTG GGA
         C   F   Y   Y   V   A   T   T   Y   F   P   L   L   P   H   P>

         245  250  255  260  265  270  275  280  285
        CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TCC CAG GGC TGC GTC
        GAG AGG ATG AAG CGG ACC GGA GAG ATG ACC CGG AGG GTC CCG ACG CAG
         L   S   Y   F   A   W   P   L   Y   W   A   C  [illegible]

         290  295  300  305  310  315  320(K)325 →129, Q508
        CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC CGC CAC CAC GCC TTC
        GAT TGG CCG CAG ACC CAG TAT CGG GTG CTC ACG GCG GTG GTG CGG AAG
         L   T   G   V   W   V   I   A   H   E   C   R   H   H   A  [illegible]

         340  345  350  355  360  365  370  375  380
        AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC
        TCG CTG ATG GTC ACC GAC CTG CTG TGG CAG CCG GAG TAG AAG GTG AGG
        [illegible]   D   T   V   G   L   I   F   H   S>

         385 390  395  400  405  410  415  420  425  430
        TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGA CGC CAC
        AAG GAG GAG CAG GGA ATG AAG AGG ACC TTC ATG TCA GTA GCT GCG GTG
         F   L   L   V   P   Y   F   S   W   K   Y   S   H   R   R   H>

         435  440  445  450  455  460  465  470  475  480
        CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG
        GTA AGG TTG TGA CCG AGG GAG CTC TCT CTG CTT CAC AAA CAG GGG TTC
         H   S   N   T   G   S   L   E   R   D   E   V   F   V   P   R>

         485  490  495  500  505  510  515  520  525
        AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG
        TTC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GAG TTG TTG GGA AAC
         K   K   S   D   I   K   W   Y   G   K   Y   L   N   N   P   L>

         530  535  540  545  550  555  560  565  570  575
        GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG
        CCT GCG TGG CAC TAC AAT TGC CAA GTC AAG TGA GAG CCG ACC GGA AAC
         G   R   T   V   M   L   T   V   Q   F   T   L   G   W   P   L>

         580  585  590  595  600  605  610  615  620
        TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT
        ATG AAT CGG AAG TTG CAG AGC CCC TCT GGA ATG CTG CCG CCG AAG CGA
         Y   L   A   F   N   V   S   G   R   P   Y   D   G   G   F   A>
```

Handwritten notes (right margin):

DNA and deduced protein sequence from virton FAD2 (B) clone

In 129 and Q508 clones (E) (A G was converted to A→G (K). This mutation was found in E clone only. But occur in both 129 and Q508 mutant lines.

Again, this region was confirmed from

EXPERIMENTER [signature] DATE

ESSED BY [signature] DATE

TITLE _cont'd_

PURPOSE _cont'd_

DATE

```
      625   630   635   640   645   650   655   660   665   670
      TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC
      ACG GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG
      C   H   F   H   P   N   A   P   I   Y   N   D   R   E   R   L>

      675   680   685   690   695   700   705   710   715   720
      CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC
      GTC TAT ATG TAG AGG CTG CGA CCG TAG GAG CGG CAG ACG ATG CCA GAG
      Q   I   Y   I   S   D   A   G   I   L   A   V   C   Y   G   L>

            725   730   735   740   745   750   755   760   765
      TAC CGC TAC GCT GCT GTC CAA GGA GTT GCC TCG ATG GTC TGC TTC TAC
      ATG GCG ATG CGA CGA CAG GTT CCT CAA CGG AGC TAC CAG ACG AAG ATG
      Y   R   Y   A   A   V   Q   G   V   A   S   M   V   C   F   Y>

      770   775   780   785   790   795   800   805   810   815
      CGA GTT CCG CTT CTG ATT GTC AAT GGG TTC TTA GTT TTG ATC ACT TAC
      CCT CAA GGC GAA GAC TAA CAG TTA CCC AAG AAT CAA AAC TAG TGA ATG
      G   V   P   L   L   I   V   N   G   F   L   V   L   I   T   Y>

      820   825   830   835   840   845   850   855   860
      TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG TCT GAG TGG
      AAC GTC GTG TGC GTA GGA AGG GAC GGA GTC ATA CTG AGC AGA CTC ACC
      L   Q   H   T   H   P   S   L   P   H   Y   D   S   S   E   W>

      865   870   875   880   885   890   895   900   905   910
      GAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC ACA GAC TAC GGA ATC
      CTA ACC AAC TCC CCT CGA AAC CGG TGG CAA CTG TCT CTG ATG CCT TAG
      D   W   L   R   G   A   L   A   T   V   D   R   D   Y   G   I>

      915   920   925   930   935   940   945   950   955   960
      TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG GCG CAT CAC
      AAC TTG TTC CAG AAG GTG TTA TAG TGC CTG TGC GTG CAC GCG GTA GTG
      L   N   K   V   F   H   N   I   T   D   T   H   V   A   H   H>

            965   970   975   980   985   990   995   1000  1005
      CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATC GAA GCT ACG AAG GCG
      GAC AAG AGC TGG TAC GGC GTA ATA GTA CGC TAG CTT CGA TGC TTC CGC
      L   F   S   T   M   P   H   Y   H   A   M   E   A   T   K   A>

      1010  1015  1020  1025  1030  1035  1040  1045  1050  1055
      ATA AAG CCG ATA CTC GGA GAG TAT TAT CAG TTG CAT GGG ACG CCG GTC
      TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAC GTA CCC TGC GGC CAG
      I   K   P   I   L   G   E   Y   Y   Q   L   H   G   T   P   V>

      1060  1065  1070  1075  1080  1085  1090  1095  1100
      GTT AAG GCG ATG TGG AGG GAG GCG AAC GAG TGT ATC TAT GTG GAA CCG
      CAA TTC CGC TAC ACC TCC CTC CGC TTG CTC ACA TAG ATA CAC CTT GGC
      V   K   A   M   W   R   E   A   K   E   C   I   Y   V   E   P>

      1105  1110  1115  1120  1125  1130  1135  1140  1145  1150
      GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA
      CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT
      D   R   Q   G   E   K   K   G   V   F   W   Y   N   N   K   L>

      1155  1160  1165  1170
      TGA AGC AAA GAA CAA ACA AT
      ACT TCG TTT CTT CTT TGT TA
      *   S   K   E   E   T   X>
```

(left strand)

(see pg 134)
for primer location

Total 5 independent
129 and 9508
clones (each white
ones) were
sequenced by
primer DR
(see page 134)
and showed the
same mutation

Thus it appears
to be true
mutation

This will be
further confirmed
by RT-PCR
RNA from 129 using
and sequence by
DR primer